REMARKS

Claims 1 and 55-58 are pending in the present application. Claims 2-54 have been cancelled. Claim 1 has been amended. Claims 55-58 are new. No new matter has been added. The claims have been rejected for lack of utility, lack of written description, and indefiniteness.

SPECIFICATION

Examiner has requested that Applicants check the specification for the use of trademarks. Applicants have reviewed the specification, and have only found the trademarks referred to by the Examiner.

Applicants submit a sequence listing to replace the current sequence listing. The sequence on page 21 has been given as SEQ ID NO:27. The specification has been amended on page 20 so that the sequence on page 21 is referred to as SEQ ID NO:27.

OBJECTION

The specification has been objected to because of the size of the font in alignments on pages 10, 11, and 21. The alignments have been changed to use larger fonts. Applicants submit that these amendments overcome the objection.

CLAIM REJECTIONS

Rejections Under 35 U.S.C. § 101

Claims 1-4 have been rejected under 35 U.S.C. § 101 as lacking support by a specific and substantial credible utility. Claims 2-4 have been cancelled, so the rejection is moot insofar as it relates to these claims. Claim 1 has been amended and claims 55-57 have been added. Applicants traverse the rejection as it applies to amended claim 1 and the new claims.

The Examiner alleges that the application does not disclose a specific biological role for SEQ ID NO:6 or its significance to a particular disease or disorder of physiological process. Further the Examiner asserts SEQ ID NO:6 has not been shown to be differentially expressed in any disease or disorder and cannot be employed in a diagnostic capacity. Therefore, according to the Examiner, the specification does not disclose a credible, substantial and specific "real world" use for SEQ ID NO:6. Applicants traverse for the reasons described below.

The requirements for satisfying the utility requirement are explained in the Manual of Patent Examination Practice (MPEP) 8th Edition, which states that only one credible assertion of specific and substantial utility, need be specified for an invention:

Specific Utility

> A "specific utility" is *specific* to the subject matter claimed. This contrasts with a *general* utility that would be applicable to the broad class of the invention. Office personnel should distinguish between situations where an applicant has disclosed a specific use for or application of the invention and situations where the applicant merely indicates that the invention may prove useful without identifying with specificity why it is considered useful. For example, indicating that a compound may be useful in treating unspecified disorders, or that the compound has "useful biological" properties, would not be sufficient to define a specific utility for the compound. Similarly, a claim to a polynucleotide whose use is disclosed simply as a "gene probe" or "chromosome marker" would not be considered to be *specific* in the absence of a disclosure of a specific DNA target. A general statement of diagnostic utility, such as diagnosing an unspecified disease, would ordinarily be insufficient absent a disclosure of what condition can be diagnosed. Contrast the situation where an applicant discloses a specific biological activity and reasonably correlates that activity to a disease condition. Assertions falling within the latter category are sufficient to identify a specific utility for the invention. Assertions that fall in the former category are insufficient to define a specific utility for the invention, especially if the assertion takes the form of a general statement that makes it clear that a "useful" invention may arise from what has been disclosed by the applicant. *Knapp v. Anderson*, 477 F.2d 588, 177 USPQ 688 (CCPA 1973).

Substantial Utility

> A "substantial utility" defines a "real world" use. Utilities that require or constitute carrying out further research to identify or reasonably confirm a "real world" context of use are not substantial utilities. For example, both a therapeutic method of treating a known or newly discovered disease and an assay method for identifying compounds that themselves have a "substantial utility" define a "real world" context of use. An assay that measures the presence of a material which has a stated correlation to a predisposition to the onset of a particular disease condition would also define a "real world" context of use in identifying potential candidates for preventive measures or further monitoring. Section 2107.01

Applicants submit that at least one substantial and specific utility exists for the claimed invention and is readily apparent based on the teachings of the specification. Applicants respectfully assert that the claimed protein, SEQ ID NO:6, is differentially expressed in the temporal cortex of Alzheimer's patients when compared to non-demented controls and is useful, *inter alia*, as a marker (diagnostic indicator) for Alzheimer's disease, thereby demonstrating a "real world" use and patentable utility (*See,* specification at page 21, line 3 to page 22, line 16, and Exhibit A, attached hereto).

In Exhibit A, included herewith, the tables depict the scaled results of quantitative gene expression analyses performed using SEQ ID NO:6 with gene-specific primers that measure the

relative SEQ ID NO:6 expression levels in normal cells or tissues, stimulated cells, or pathological tissue samples. The Relative Expression Score for each sample indicates the relative quantity of a SEQ ID NO:6 transcript, with 0.0 indicating no detectable expression and 100.00 indicating highest detectable expression level.

Exhibit A shows that SEQ ID NO:6 is found to be down-regulated in the temporal cortex of Alzheimer's disease patients when compared with non-demented controls ($p = 0.0003$ when analyzed by Ancova, estimate of total cDNA loaded per well used as a covariate). Therefore, it would be obvious to one of skill in the art, that SEQ ID NO:6 would be useful, for example, in screening individuals for Alzheimer's disease. (Table AC. CNS_neurodegeneration_v1.0).

Applicants assert that the specification and accompanying Exhibit A identifies a disease/disorder associated with SEQ ID NO:6, shows differential expression of the protein in the disease/disorder which one skilled in the art would recognize as useful in identifying subjects with Alzheimer's disease and thus have a credible, specific and substantial utility. Applicants thus respectfully request withdrawal of the rejection under 35 U.S.C. §101.

Rejections under U.S.C. § 112, first paragraph

Claims 1-4 were rejected under 35 U.S.C. § 112, first paragraph because one skilled in the art would not know how to use the invention since the claimed invention lacks utility. Claims 2-4 have been cancelled, so the rejection is moot insofar as it relates to these claims. Claim 1 has been amended. As discussed above, throughout the specification and Exhibit A, Claim 1 has a specific, substantial, and credible utility. Since this claim has been demonstrated to have such utility, Applicants submit that this rejection should be withdrawn.

Claims 1-4 were also rejected under 35 U.S.C. § 112, first paragraph for lack of written description. Claims 2-4 have been cancelled, so the rejection is moot insofar as it relates to these claims. Examiner alleges that the specification contains no description of a mature or variant form of SEQ ID NO:6. Further, Examiner alleges that the instant specification does not identify those structural features in SEQ ID NO:6 which are found only in the genus of proteins defined by the structural limitations of these claims.

To facilitate prosecution, Applicants have amended claim 1 to an amino acid sequence comprising SEQ ID NO:6. Applicants have also added new claim 57, which recites an amino acid at least 99% identical to SEQ ID NO:6. Applicants assert that the amino acid alignments

between SEQ ID NO:6 and KIAA1246 provide guidance as to which amino acids are critical to conserve and which are not within 99% identity to SEQ ID NO:6.

New claim 56 refers to a polypeptide cleaved of its signal peptide, comprising amino acids 17-628. Support for this claim can be found on page 17, lines 11-13 of the specification. Page 2 of the specification teaches that the mature form of a polypeptide can be formed by the cleavage of a signal sequence as described on page 17 of the specification. Applicants submit that this is sufficient description to satisfy the written description requirement. Therefore, Applicants request that this rejection be withdrawn.

Rejections under U.S.C. § 112, second paragraph

Claims 1-4 were rejected under 35 U.S.C. § 112, second paragraph for indefiniteness. Claims 2-4 have been cancelled, so the rejection is moot insofar as it relates to these claims. Applicants have amended claim 1 as mentioned above to read on only an amino acid sequence comprising SEQ ID NO:6. Claim 1 no longer recites the indefinite language. Therefore, Applicants request that this rejection be withdrawn.

CONCLUSION

On the basis of the foregoing amendments, Applicants respectfully submit that the pending claims are in condition for allowance. If there are any questions regarding these amendments and remarks, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,

Ivor R. Elrifi, Reg. No. 39,529
Attorney for Applicant
c/o Mintz, Levin
One Financial Center
Boston, MA 02111
Telephone: (617) 542 6000
Fax: (617) 542 2241

Dated: April 4, 2003

Exhibit A

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on an Applied Biosystems ABI PRISM® 7700 or an ABI PRISM® 7900 HT Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on metabolic diseases), AI_comprehensive_panel (containing normal tissue and samples from autoinflammatory diseases), Panel CNSD.01 (containing samples from normal and diseased brains) and CNS_neurodegeneration_panel (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β-actin and GAPDH). Normalized RNA (5 ul) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (Applied Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions.

In other cases, non-normalized RNA samples were converted to single strand cDNA (sscDNA) using Superscript II (Invitrogen Corporation; Catalog No. 18064-147) and random hexamers according to the manufacturer's instructions. Reactions containing up to 10 μg of total RNA were performed in a volume of 20 μl and incubated for 60 minutes at 42°C. This reaction can be scaled up to 50 μg of total RNA in a final volume of 100 μl. sscDNA samples are then normalized to reference nucleic acids as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions.

Probes and primers were designed for each assay according to Applied Biosystems Primer Express Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (Tm) range = 58°-60°C, primer optimal Tm = 59°C, maximum primer difference = 2°C, probe does not have 5'G, probe Tm must be 10°C greater than primer Tm, amplicon size 75bp to 100bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final concentrations were: forward and reverse primers, 900nM each, and probe, 200nM.

PCR conditions: When working with RNA samples, normalized RNA from each tissue and each cell line was spotted in each well of either a 96 well or a 384-well PCR plate (Applied Biosystems). PCR cocktails included either a single gene specific probe and primers set, or two multiplexed probe and primers sets (a set specific for the target clone and another gene-specific set multiplexed with the target probe). PCR reactions were set up using TaqMan® One-Step RT-PCR Master Mix (Applied Biosystems, Catalog No. 4313803) following manufacturer's instructions. Reverse transcription was performed at 48°C for 30 minutes followed by amplification/PCR cycles as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

When working with sscDNA samples, normalized sscDNA was used as described previously for RNA samples. PCR reactions containing one or two sets of probe and primers were set up as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions. PCR amplification was performed as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were analyzed and processed as described previously.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on these panels are comprised of samples derived from all major organ systems from single adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var = small cell variant,
non-s = non-sm = non-small,
squam = squamous,
pl. eff = pl effusion = pleural effusion,

glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

Panel CNS_Neurodegeneration_V1.0

The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically senile plaque load rated as level 3 on a scale of 0-3; 0 = no evidence of plaques, 3 = severe AD senile plaque load). Within each of these brains, the following regions are represented: hippocampus, temporal cortex (Brodman Area 21), parietal cortex (Brodman area 7), and occipital cortex (Brodman area 17). These regions were chosen to encompass all levels of neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the parietal cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within AD patients. Not all brain regions are represented in all cases.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology upon autopsy
Control = Control brains; patient not demented, showing no neuropathology
Control (Path) = Control brains; pateint not demented but showing sever AD-like pathology
SupTemporal Ctx = Superior Temporal Cortex
Inf Temporal Ctx = Inferior Temporal Cortex

A. Results

Expression of gene CG53944-01 was assessed using the primer-probe sets Ag2639 and Ag2641, described in Tables AA and AB. Results of the RTQ-PCR runs are shown in Tables AC and AD.

Table AA. Probe Name Ag2639

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctcatcctcagcaacaacca-3'	20	406	
Probe	TET-5'-cctggatgattgtgccgagacact-3'-TAMRA	24	450	

Reverse	5'-taggagaggtcgaggtcctc-3'	20	475	

Table AB. Probe Name Ag2641

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctcatcctcagcaacaacca-3'	20	406	
Probe	TET-5'-cctggatgattgtgccgagacact-3'-TAMRA	24	450	
Reverse	5'-tgtaggagaggtcgaggtcc-3'	20	477	

Table AC. CNS_neurodegeneration_v1.0

Column A - Rel. Exp.(%) Ag2641, Run 206954924			
Tissue Name	A	Tissue Name	A
AD 1 Hippo	21.6	Control (Path) 3 Temporal Ctx	13.6
AD 2 Hippo	51.1	Control (Path) 4 Temporal Ctx	48.6
AD 3 Hippo	10.1	AD 1 Occipital Ctx	11.9
AD 4 Hippo	18.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	9.4
AD 6 Hippo	58.6	AD 4 Occipital Ctx	15.4
Control 2 Hippo	38.4	AD 5 Occipital Ctx	19.8
Control 4 Hippo	20.6	AD 6 Occipital Ctx	39.2
Control (Path) 3 Hippo	11.3	Control 1 Occipital Ctx	11.3
AD 1 Temporal Ctx	17.0	Control 2 Occipital Ctx	79.0
AD 2 Temporal Ctx	43.8	Control 3 Occipital Ctx	25.3
AD 3 Temporal Ctx	13.6	Control 4 Occipital Ctx	12.9
AD 4 Temporal Ctx	23.8	Control (Path) 1 Occipital Ctx	81.2
AD 5 Inf Temporal Ctx	82.4	Control (Path) 2 Occipital Ctx	22.4
AD 5 SupTemporal Ctx	46.7	Control (Path) 3 Occipital Ctx	9.0
AD 6 Inf Temporal Ctx	57.8	Control (Path) 4 Occipital Ctx	37.4
AD 6 Sup Temporal Ctx	51.4	Control 1 Parietal Ctx	11.7
Control 1 Temporal Ctx	15.5	Control 2 Parietal Ctx	47.0
Control 2 Temporal Ctx	66.9	Control 3 Parietal Ctx	29.1
Control 3 Temporal Ctx	29.9	Control (Path) 1 Parietal Ctx	84.1
Control 4 Temporal Ctx	22.5	Control (Path) 2 Parietal Ctx	31.0
Control (Path) 1 Temporal Ctx	51.1	Control (Path) 3 Parietal Ctx	9.5
Control (Path) 2 Temporal Ctx	31.2	Control (Path) 4 Parietal Ctx	60.7

Table AD. Panel 1.3D

Column A - Rel. Exp.(%) Ag2639, Run 157543474			
Tissue Name	A	Tissue Name	A
Liver adenocarcinoma	17.1	Kidney (fetal)	4.0

Pancreas	2.7	Renal ca. 786-0	1.9
Pancreatic ca. CAPAN 2	3.9	Renal ca. A498	15.2
Adrenal gland	4.4	Renal ca. RXF 393	1.4
Thyroid	5.9	Renal ca. ACHN	2.9
Salivary gland	7.0	Renal ca. UO-31	3.4
Pituitary gland	16.5	Renal ca. TK-10	1.6
Brain (fetal)	12.4	Liver	2.9
Brain (whole)	12.4	Liver (fetal)	2.3
Brain (amygdala)	31.0	Liver ca. (hepatoblast) HepG2	5.3
Brain (cerebellum)	11.2	Lung	7.3
Brain (hippocampus)	**100.0**	Lung (fetal)	5.1
Brain (substantia nigra)	3.6	Lung ca. (small cell) LX-1	1.5
Brain (thalamus)	19.3	Lung ca. (small cell) NCI-H69	9.2
Cerebral Cortex	24.1	Lung ca. (s.cell var.) SHP-77	7.3
Spinal cord	5.9	Lung ca. (large cell)NCI-H460	3.3
glio/astro U87-MG	12.9	Lung ca. (non-sm. cell) A549	18.0
glio/astro U-118-MG	17.1	Lung ca. (non-s.cell) NCI-H23	7.0
astrocytoma SW1783	10.4	Lung ca. (non-s.cell) HOP-62	7.3
neuro*; met SK-N-AS	27.7	Lung ca. (non-s.cl) NCI-H522	4.4
astrocytoma SF-539	9.9	Lung ca. (squam.) SW 900	4.4
astrocytoma SNB-75	19.9	Lung ca. (squam.) NCI-H596	0.6
glioma SNB-19	11.2	Mammary gland	9.5
glioma U251	2.2	Breast ca.* (pl.ef) MCF-7	6.3
glioma SF-295	11.2	Breast ca.* (pl.ef) MDA-MB-231	48.3
Heart (fetal)	5.4	Breast ca.* (pl.ef) T47D	0.7
Heart	1.0	Breast ca. BT-549	13.9
Skeletal muscle (fetal)	15.3	Breast ca. MDA-N	8.5
Skeletal muscle	1.5	Ovary	10.4
Bone marrow	1.2	Ovarian ca. OVCAR-3	7.2
Thymus	2.2	Ovarian ca. OVCAR-4	1.7
Spleen	7.4	Ovarian ca. OVCAR-5	3.6
Lymph node	2.4	Ovarian ca. OVCAR-8	3.7
Colorectal	1.5	Ovarian ca. IGROV-1	2.5
Stomach	7.1	Ovarian ca.* (ascites) SK-OV-3	3.5
Small intestine	12.8	Uterus	14.6
Colon ca. SW480	7.4	Placenta	3.4
Colon ca.* SW620(SW480 met)	3.0	Prostate	5.7
Colon ca. HT29	2.5	Prostate ca.* (bone met)PC-3	5.6

Colon ca. HCT-116	5.9	Testis	10.2
Colon ca. CaCo-2	5.0	Melanoma Hs688(A).T	5.3
Colon ca. tissue(ODO3866)	6.7	Melanoma* (met) Hs688(B).T	3.1
Colon ca. HCC-2998	23.2	Melanoma UACC-62	2.0
Gastric ca.* (liver met) NCI-N87	9.9	Melanoma M14	2.8
Bladder	1.2	Melanoma LOX IMVI	15.0
Trachea	12.6	Melanoma* (met) SK-MEL-5	3.1
Kidney	1.2	Adipose	2.0

CNS_neurodegeneration_v1.0 Summary: Ag2641 This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. This gene is found to be down-regulated in the temporal cortex of Alzheimer's disease patients patients when compared with non-demented controls ($p = 0.0003$ when analyzed by Ancova, estimate of total cDNA loaded per well used asa covariate). Therefore, up-regulation of this gene or its protein product, or treatment with specific agonists for this receptor may be of use in reversing the dementia, memory loss, and neuronal death associated with Alzheimer's disease.

Panel 1.3D Summary: Ag2639 Highest expression is seen in the hippocampus (CT=26.3). In addition, high to moderate levels of expression are seen in all regions of the CNS examined, including amygdala, hippocampus, substantia nigra, thalamus, and hypothalamus. This expression suggests that therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.